If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

On page 24, paragraph beginning at line 10:

The EMF1 gene (GenBank accession number: AF319968) encodes a predicted 121.7 kDA protein [(Figure 2A)] with similarity to two *Arabidopsis* EST clones (GenBank accession number N96450 and Z46543) and to a hypothetical protein from the rice genomic sequencing project (GenBank accession number BAA94774.1[, Figure 2]).

On page 24, paragraph beginning at line 14:

To better characterize the rice EMF1 homolog (OsEMF1), we isolated the corresponding cDNA clone by the rapid amplification of cDNA ends (RACE) technique. The OsEMF1 cDNA of 3896 nucleotides (GenBank accession number AF326768) predicts a 1057 amino acid polypeptide (estimated molecular weight, 116.4 kDA) that is 328 amino acids shorter than the predicted protein in BAA94774.1. The organization of introns and exons predicted at the 5' end in BAA94774.1 was not confirmed by the sequence of the OsEMF1 cDNA [(Figure 2A)]. The OsEMF1 cDNA is likely to include a complete open reading frame because several stop codons are found in all the three possible reading frames upstream of a first ATG initiating the 1057 amino acid polypeptide. The *Arabidopsis* and *Oryza* predicted protein sequences display 37% similarity and 20% identity over their entire length.

On page 24, paragraph beginning at line 26:

Neither EMF1 nor OsEMF1 displays significant homology to proteins of known function from any organism. Nevertheless, several domains could be identified in the predicted EMF1 and OsEMF1 polypeptides [(Figure 2B)], including nuclear localization signals (Raikhel, 1992), phosphorylation sites, an ATP/GTP binding motif (P-loop) (Walker et al., 1982), and a LXXLL motif. The LXXLL motif has been demonstrated to mediate the binding of steroid receptor co-activator complexes to a nuclear receptor ((Heery et al. Nature, 387:733 (1997); Torchia et al., 1997). In plants, it has been identified in the RGA and GAI proteins, both transcriptional regulators in the gibberellic acid (GA) signal transduction pathway (Peng et al., 1997; Silverstone et al., Plant Cell, 10: 155 (1998)). A PSI-BLAST homology search (Altschul et al., 1997) indicates a region of the EMF1 protein between amino acids 901 and 1034 that displays similarity (identities: 23%, positives: 37%) with two members of a nuclear receptor gene family. This gene family comprises one of the most abundant groups of transcriptional regulators in mammals with members involved in various developmental processes (Sluder et al., 1999).

Furthermore, the EMF1 protein displays homopolymeric stretches of serine residues, as do the two transcriptonal regulators RGA and GAI, (Silverstone et al., Plant Cell, 10: 155 (1998)). The identification of these motifs indicates that EMF1 and OsEMF1 could represent a new class of regulatory molecules that function as transcriptional regulators during shoot development in higher plants.